

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	United States of America
Main trait group¹ NOTE! Only one trait group per form!	Direct (single-trait) and combined (multi-trait) longevity.
Breed(s)	AYS, BSW, GUE, JER, HOL (B&W and R&W), MSH
Trait definition(s) and unit(s) of measurement² Attach an appendix if needed	Productive life: Time in the milking herd before removal by voluntary culling, involuntary culling, or death. Credits for each month in milk are obtained from standard lactation curves and are then summed across all lactations. Diminishing credits within lactation give cows more credit for beginning a new lactation than for continuing to milk in the previous lactation. Cows get 8 months credit for 305-d first lactation records, 10 months credit for second lactations, 10.2 months credit for third and later lactations, partial credits for shorter records, and extra credits for longer records.
Method of measuring and collecting data	Calving dates, disposal dates, reasons for disposal, and lactation lengths are obtained from DHI data. Dead cows receive credit for months of production as stated above. Live cows receive additional credit for predicted remaining life expectancy. Prediction factors consider the cow's age and stage of lactation. Credits from more than one herd are combined for cows that change herds. Published productive life combines information from direct longevity with evaluations from correlated traits.
Time period for data inclusion	Birth year 1950 and later for pedigree, 1960 and later for first calving. Cows must be born at least 3 years prior to the evaluation to be included.
Age groups (e.g. parities) included	All parities.
Other criteria (data edits) for inclusion of records	Cows must be sire identified with first lactation records.
Criteria for extension of records (if applicable)	Records are extended for cows that are still alive, were sold for dairy purposes, or were in herds that discontinued testing. Cows sold for dairy purposes or in herds that discontinued testing receive extended records if they had opportunity to reach 3 years of age; otherwise their records are discarded.
Sire categories	All sires.
Environmental effects³, pre-adjustments	Genetic variance in censored and uncensored management groups is equalized by pre-adjusting censored data using expansion factors.
Method (model) of genetic evaluation³	Single-trait BLUP animal model. Records from censored management groups receive less weight than from uncensored.

Environmental effects³ in the genetic evaluation model	Fixed: management group (flexible-length groups are based on herd of first lactation and birth date. Registry status is also considered for Holsteins only), regression on inbreeding. This model produces PTA adjusted to 0 inbreeding, but published PTA include the regression multiplied by expected future inbreeding (EFI) as a post-processing step. Random: Sire-by-herd interaction (variance = 5% of phenotypic variance).
Adjustment for heterogeneous variance in evaluation model	None.
Use of genetic groups and relationships	Unknown dams of cows, sires of cows, and parents of sires are grouped separately by birth year. Complete relationship matrix accounting for inbreeding.
Blending of foreign/Interbull information in evaluation	Direct longevity for foreign bulls is combined with PTA for other traits using the same multi-trait procedures used for domestic bulls.
Genetic parameters in the evaluation	Heritability is 8%. After the direct longevity evaluation, information from 10 other traits and composites is combined by selection index theory to increase PL reliability. These traits include yield, somatic cell score (SCS), daughter pregnancy rate (DPR), service sire calving ease (SCE), daughter calving ease (DCE) and three conformation composites. Correlations with PL are: Milk .08 Fat .08 Protein .10 SCS -.38 DPR .51 SCE -.25 DCE -.30 Composites: Udder .30 Feet & leg .19 Size -.16 The selection index procedures use the predicted transmitting abilities, parent averages, and reliabilities of PTA and PA for the 11 traits and are applied to both bulls and cows in age order so that improved PL evaluations of parents are transferred to their progeny.
System validation	Direct PL is obtained with the same animal model programs used for yield. Combined PL programs produced evaluations similar to MACE when tested on international yield data. Trend validation methods 2 and 3 are applied.
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	PTA

Definition of genetic reference base	Five year stepwise base: average of all cows born in 2000 is set to 0.
Next base change	Next base change in February 2010, when the base will be cows born in 2005.
Calculation of reliability	A daughter that has had the opportunity to reach 8 years of age is considered a completed observation and gets 1 daughter equivalent. Cows with less opportunity get less DE regardless of whether they are culled or alive. The DE are .22 at 36 months of age, .53 at 48 mo, .75 at 60 mo, .89 at 72 mo, and .95 at 84 mo. These DE are combined with DE from parent average to calculate direct REL, and then DE from other traits increase the combined REL.
Criteria for official publication of evaluations	All bulls evaluated for milk yield by USA or by Interbull have official PL evaluations. Interbull longevity evaluations are used if the bull has foreign daughters and if the Interbull reliability is higher than the single-trait domestic longevity evaluation.
Number of evaluations / publications per year	Four, in February, May, August, and November.
Use in total merit index⁴	Net Merit (all breeds): PL receives 11% of the total emphasis. TPI (Holsteins): PL receives 8% of the total emphasis.
Anticipated changes in the near future	An all-breed model including crossbred cows.
Key reference on methodology applied	<p>VanRaden, P.M. and E.J.H. Klaaskate. 1993. Genetic evaluation of length of productive life including predicted longevity of live cows. J. Dairy Sci. 76:2758-2764.</p> <p>VanRaden, P.M. and G.R. Wiggans. 1995. Productive life evaluations: calculation, accuracy, and economic value. J. Dairy Sci. 78:631-638.</p> <p>VanRaden, P.M. 2001. Methods to combine estimated breeding values obtained from separate sources. J.Dairy Sci. 84:E47-E55</p> <p>VanRaden, P.M., C. M. B. Dematawewa, R. E. Pearson and M. E. Tooker. 2006. Productive Life including all lactations and longer lactations with diminishing credits. J.Dairy Sci. (accepted).</p>
Key organisation: name, address, phone, fax, e-mail, web site	<p>Animal Improvement Programs Laboratory USDA, Agricultural Research Service Building 005, Room 306, BARC-West 10300 Baltimore Avenue Beltsville, Maryland 20705-2350 U.S.A. Tel: 301-504-8334 Fax: 301-504-8092 E-mail: paul@aipl.arsusda.gov web site: http://aipl.arsusda.gov</p>

1) Either: Production (e.g. milk, fat, protein), Conformation, Health (e.g. mastitis resistance, milk somatic cell, resistance to diseases other than mastitis), Longevity, Calving (e.g. stillbirth, calving ease), Female fertility (e.g. non-return rate, interval between reproductive events, number of AI's, heat strength), Workability (e.g. milking speed, temperament), Beef production, Efficiency (e.g. body weight, energy balance, body conditioning score), or Other traits.

2) Indicate frequencies per category if the trait is categorical and specify transformation of data if practiced.

- 3) Use abbreviations for most common effects (see document with list of abbreviations at http://www-interbull.slu.se/service_documentation/General/list_of_abbreviations.rtf) and indicate random (R) or fixed (F).
- 4) Please give economic weights and indicate how they are expressed (preferably in genetic standard deviation units).

Parameters for national genetic evaluations for longevity traits as provided to Interbull

Country (or countries):

Main trait group: Longevity

Breed(s):

Trait	h^2	genetic variance	official proof standardisation formula ^a
Direct longevity:	.08	19.63	None
Combined longevity:	.08	19.63	None

^a Expressed as follows:
 $\text{StandEval} = ((\text{eval} - a) / b) * c + d$ where a=mean of the base adjustment, b=standard deviation of the base, c=standard deviation of expression (include sign if scale is reversed), and d=base of expression.